

Abstract of Disclosure

[0039] There is a tremendous need for high throughput gene expression technology which can efficiently and cheaply identify and accurately isolate different genes expressed between diseased and normal tissues for use in discovering new drugs. The present invention utilizes a combination of biomolecular chemistry methods to eliminate/degrade redundant sequences and fluorescence dye assay to identify these unique sequences from two cell or tissue populations. cDNA from normal or diseased cells or tissues are hybridized with the RNA of the complement normal or diseased cells or tissues. The hybridized cDNA/RNA is incubated with exonucleases, resulting in degradation of all but the single stranded RNA and DNA. RNA are then eliminated using RNase and the remaining DNA which are unique to the sample are amplified. This technique may be used to isolate differentially expressed genes or gene fragments and will provide a means to isolate and identify medium to low gene expressions that may otherwise be buried under gene "noise".